

## Poster III-8

### **The Genetic Association Database**

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Genome sequencing projects, as well the accumulation of genetic variation information through SNP projects and other sources, have resulted in a large amount of human polymorphism data. In parallel, many groups have used genetic association studies to identify clinically relevant polymorphisms. The genetic association database (GAD) is a public archive of published gene based genetic association studies that allows querying of human genetic variation in the context of allelic, phenotypic, and disease relevance. GAD currently contains data from over 1,500 published genetic associations studies. GAD is organized with information relevant to gene based molecular annotation, allelic information, study parameters including population and study size, as well as statistical significance. Importantly, this includes studies resulting statistically significant associations, as well as those with a lack of association. This database has simple, advanced and batch search capabilities. Importantly, the batch search capability allows rapid integration of data produced by microarray, proteomic, or other high throughput systems. This web based publicly available database will aid in the systematic analysis of gene variation in the context of biological, polymorphic, and clinical relevance. <http://geneticassociationdb.nih.gov>